

Appl. No. To Be Assigned; Group Art Unit: To Be Assigned  
 Dkt. No. 0610.005000/IMAC;  
 Inventor(s): Robinson et al.; Tel: 202/371-2600  
 Title: Modular Assembly of Antibody Genes, Antibodies  
 Prepared Thereby and Use

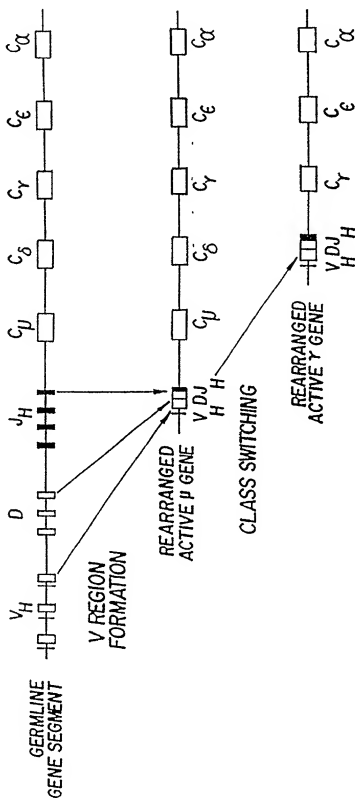


FIG. 1

Ig heavy chain J-C regionhuman heavy chain J regions

J|CH1

JH1 GCTGAATACTTCCAGCACTGGGGCCAGGGCACCCCTGGTCACCGTCTCCTCAG  
 JH2 CTACTGGTACTTCGATGTCTGGGGCCCTGGCACCCCTGGTCAGTGTCTCCTCAG  
 JH3 ATGCTTTTGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCAG  
 JH4 ACTACTTTGACTACTGGGGCCAAGGAACCCCTGGTCACCGTCTCCTCAG  
 JH5 ACACTGGTTCGACTCTCTGGGGCCAAGGAACCCCTGGTCACCGTCTCCTCAG  
 JH6 AT(TAC)<sub>5</sub>GGTATGGACGTCTGGGGGCCAAGGGACACCGTACCGTCTCCTCAG  
Consensus TCGACCTCTGGGGCCAAGGAACCCCTGGTCACCGTCTCCTCAG

mouse heavy chain J regions

J|CH1

JH1 TACTGGTACTTCGATGTCTGGGGGCCAGGGACACCGTACCGTCTCCTCAG  
 JH2 TACTTTGACTACTGGGGCCAAGGCACCACTCTCAGTCTCCTCAG  
 JH3 CCTGGTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCAG  
 JH4 TACTATGCTATGGAAGTCTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAG  
Consensus TTTGACTACTGGGGCCAAGGGACACCGTACCGTCTCCTCAG

Ig light chain J-C regionhuman Kappa J region

J|C

JK1 GGACGTTTCGGCCAAGGGACCAAGGTGGAAATCAAAC  
 JK2 ACACTTTTCGGCCAGGGACCAAGCTGCAGATCAAAC  
 JK3 TCACTTTCGGCCCTGGGACCAAGGTGGATATCAAAC  
 JK4 TCACTTTCGGCCGAGGGACCAAGGTGGAGATCAAAC  
 JK5 TCACCTTCGGCCAAGGGACACGACTGGAGATTAAAC  
Consensus TTCGGCCAAGGGACCAAGGTGGAGATCAAAC

mouse Kappa J region

J|C

JK1 TGGACGTTTCGGTGGAGGACCAAGCTGGAATCAAAC  
 JK2 TACACGTTTCGGAGGGGGGACCAAGCTGGAATAAAAC  
 JK3 TTCACATTCACTGATGGGACCAAGCTGGAATAAAAC  
 JK4 TTCACGTTTCGGTTCGGGGACCAAGCTGGAATAAAAC  
 JK5 CTCACGTTTCGTTCTGGGACCAAGCTGGAGCTGAAAC  
Consensus TTCGGTGGGGGGACCAAGCTGGAATAAAAC  
 UIG[MJK] TGGTTGACCTTTATTTTG

human Lambda pseudo J region

J|C

JPSL1 CACATGTTTGGCAGCAAGACCCAGCCCACTGTCTTAG

mouse Lambda J region

J|C

JL1 TGGGTGTTTCGGTGGAGGAACAACTGACTGTCTCTAG  
 JL2 TATGTTTTTCGGCGGTGGAACCAAGGTCACTCTCTAG  
 JL3 TTTATTTTCGGCAGTGGAAACCAAGGTCACTGTCTCTAG  
Consensus TTCGGCGGTGGAACCAAGGTCACTGTCTCTAG

FIG. 2

10040945-010902

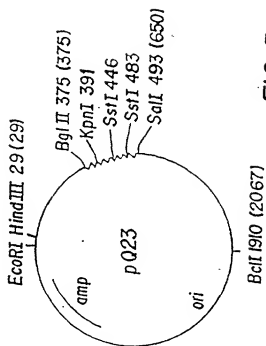


FIG. 5

Appl. No. To Be Assigned, Group Art Unit. To Be Assigned  
 Dkt. No. 061005000/MAC  
 Inventor(s): Robinson et al.; Tel: 202/371-2600  
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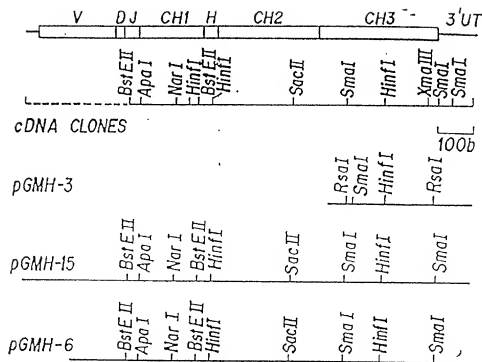


FIG. 4A

Appl. No. To Be Assigned; Group Art Unit: To Be Assigned  
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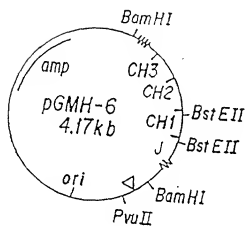


FIG. 4B

10043945-010902

Appl. No. To Be Assigned: Group Art Unit: To Be Assigned  
 Dist. No. 0610.0030000/MAC  
 Inventor(s): Robinson et al; Tel: 202/371-2600  
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 Prepared Thereby and Use

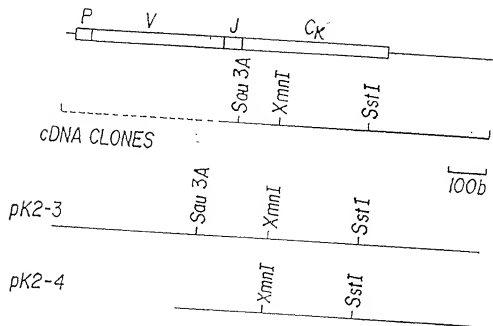


FIG. 6A

Appl. No. To Be Assigned; Group Art Unit: To Be Assigned  
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 Prepared Therapy and Use

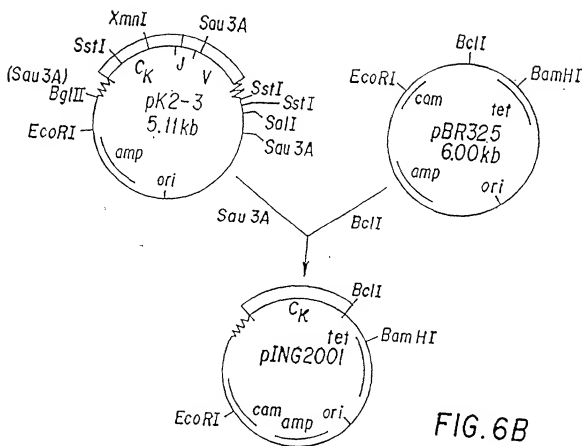


FIG. 6B

## IgG1 HEAVY CHAIN J-C REGION

HUMAN IgG1 pGMH-6  
 — J REGION — | — IgG1 CH1 REGION —  
 GGTCACGGTCTCCTCAG CCTCCACCAAGGGCCCATC  
 BstEII

## MOUSE HEAVY CHAIN J REGIONS AND PRIMERS

		MISMATCHES				
		N	JH1	JH2	JH3	JH4
JH1 TACTGGTACTTCGATGCTCTGGGGGGCCAGGACCAACGGTCACGGTCTCCTCAG [MJH1]	GCCAGTGGCAGAGGATCGGT	21	0	4	4	1
JH2 TACTTTGACTACTGGGGCCAGGACCACTCTCACAGTCTCCTCAG [MJ21]	GAGAGTGTACAGACGAGTCGGT	21	4	1	7	4
JH3 CCTGGTTTGCTTACTGGGGCCAGGACTCTGGTCACTGTCTCTGCAG [MJH3]	ACCAGTGACAGACGTCGGT	21	4	7	0	5
[MJH3-BSTE11]	TCCCTGAGACCAAGTGGCAGAG	21	3	7	1	5
[MJH3-BSTE11(13)]	ACCAGTGGCAGAG BstEII	13	1	4	1	2
JH4 TACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACGGTCTCCTCAG [MJH4]	GTCAGTGGCAGAGGATCGGT	21	1	4	5	0

FIG. 7A



Ig KAPPA CHAIN J-C REGION		-J REGION — —1gK CONSTANT REGION—			
HUMAN KAPPA pK2-3		CTGGAGATGAAC GAACGTGGCTGCACCATCTGCTTCACTTCC			
pING2016E		TGATCAAC GAACGTGGCTGCACCATCTGCTTCACTTCC			
		<u>BclI</u>			
MOUSE HEAVY KAPPA J REGIONS AND PRIMERS				MISMATCHES	
JK1 TGGACGTTGGTGGAGGACCAAGCTGGAATCAAAC					
[5JK1] GCAAGCCACCTCCGTTG					
JK2 TACACGTTGGAGGGGACCAAGCTGGAAATAAAAC					
[JK2BGLI1] CCTGGTTGGACCTCTAGATT					
[5JK2] GTCAAGCCCTCCGCCCTGG					
		<u>BglII</u>			
JK4 TTCACGTTGGCTCGGGGACAAAGTTGGAATAAAAC					
[5JK4] GCAAGCCGAGCCCTGT					
[JK4BGLI1] GCCCGTGTTCACGCTCTAGATT					
		<u>BglII</u>			
JK5 CTCACGTTGGTGGGACCAAGTGGAGCTGAAC					
[5JK5] GCAAGCCACGACCTGG					
[MUK] TGGTGGACCTTTATTTTG					

FIG.7B

# MOUSE VARIABLE REGION CONSENSUS PRIMERS

## MOUSE HEAVY CHAIN J SEGMENTS

JH1 TACTGGTACTTCGATGCTCTGGGGCGCAGGGACCAC GGTCACC GTCTCCTCA  
 JH2 TACITTTGACTACTGGGGCCAAGGCACCAC GTCTCCTCA  
 JH3 CCTGGTTTGCTTACTGGGGCCAAGGGAATGG GTCTCTGCA  
 JH4 TACTATGCTATGGACTACTGGGGTCAAGCAACCTC GTCTCCTCA

CONSENSUS PRIMER: UIG-H AGGGACCAC GGTCACC GTCTC

BsIEII  
 TCCCTGGTG CCACTGG CAGAG  
 3' 5'

## MOUSE LIGHT CHAIN J SEGMENTS

JK1 TGGACGTTCCGGTGAGGACC AAGCTG GAAATCAAA  
 JK2 TACACGTTCCGAGGGGGGACC AAGCTG GAAATAAAA  
 JK4 TTCACGTTCCGCTCGGGGAC AAGCTG GAAATAAAA  
 JK5 CTCACGTTCCGTGCTGGGACC AAGCTG GAGCTGAAA

CONSENSUS PRIMER: UIG-K GGGACC AAGCTT GAG

HindIII  
 CCCTGG TTCGAA CTC  
 3' 5'

pGML60

GGAGGGACC AAGGTG GAGATGAAA  
 -----C-T-----  
 HindIII

FIG.7C

## MOUSE $\gamma$ 2a J/C JUNCTION PRIMER

MJH2-ApaI TGTGAGAGGAGTCGGTCGTGTTCCCGGTA  
 3' ApaI 5'

FIG.7D

10040345.010902

# HEAVY CHAIN V REGION MODULE GENE SYNTHESIS

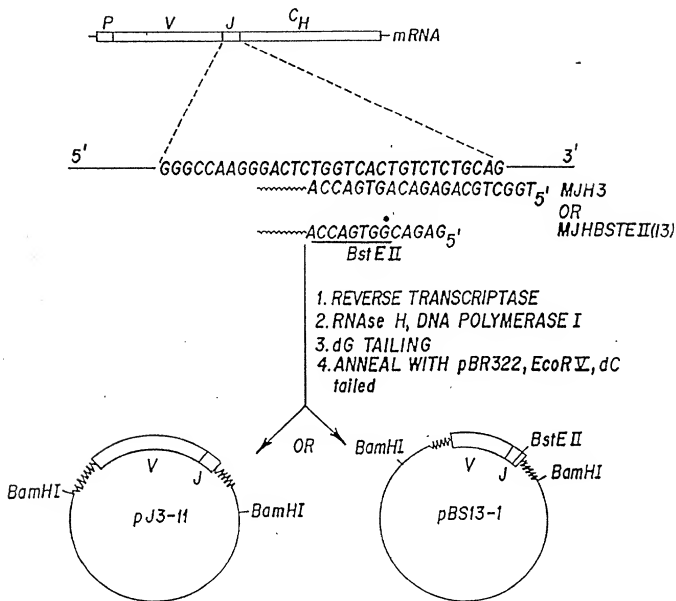


FIG. 8

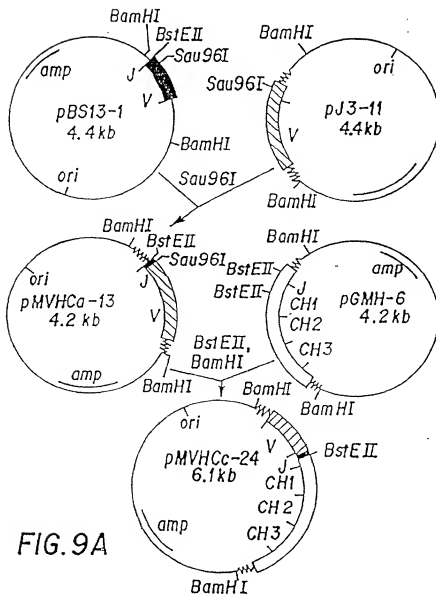


FIG. 9A

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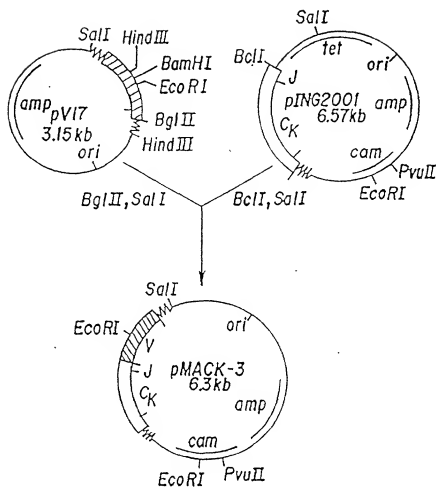


FIG. 9B

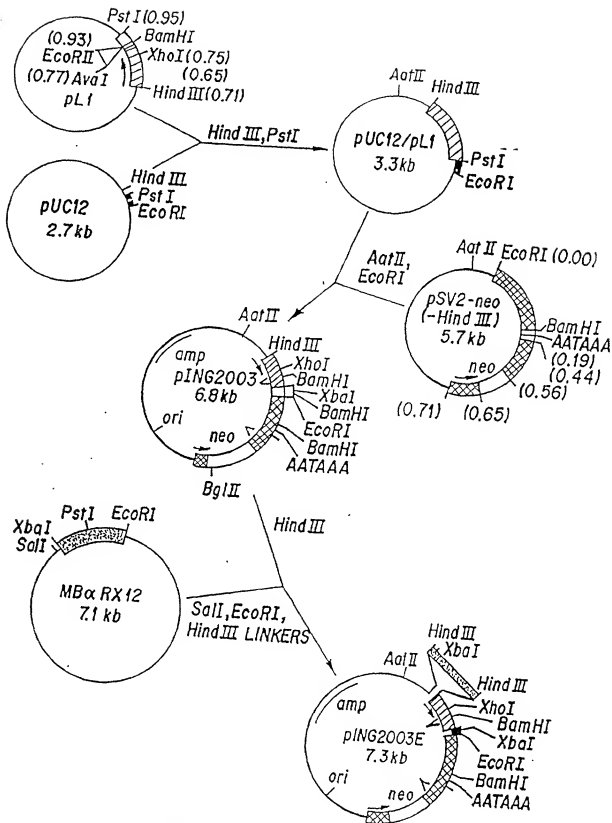


FIG. 10

10040945.010902

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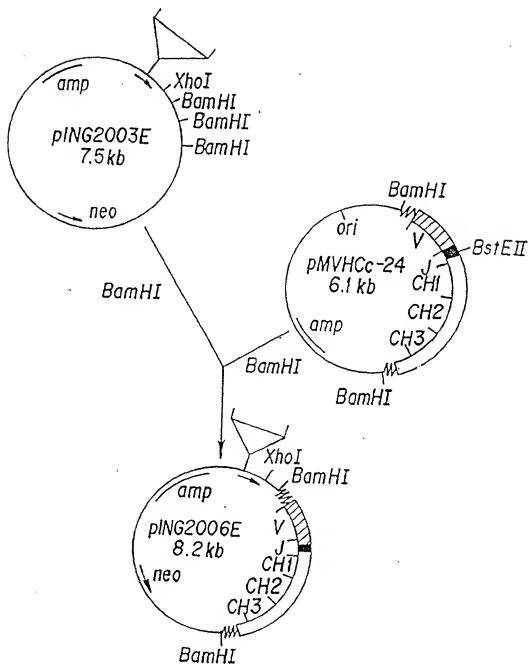


FIG. 11

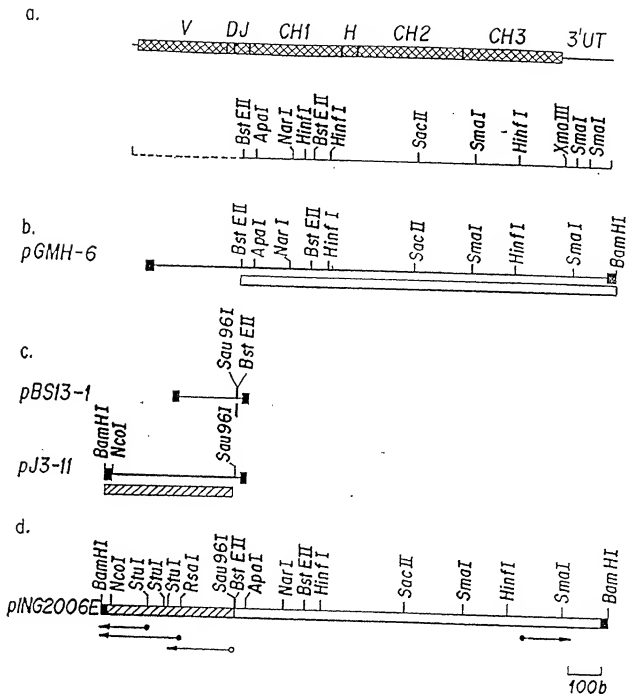


FIG.12A



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pING2006E MET Gly Trp Ser Tyr Ile Ile Leu Phe Leu Val Ala Thr Ala Arg Asp  
 pING2012E GGA TCC<sub>4</sub>CCC ACC ATG GGA TGG AGC TAT ATC ATC CTC TTT TTG GTA GCA ACA GCT AGA GAT  
 GTC TCT CTC GAC ATG 2 30 45 60  
 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser  
 GTC CAC TCC CAG CTC CAA TTG CAG CAG CCT GCG GCT GAA CTG CTG AAA CCT GGG GCT TCA  
 75 90 105 120 17  
 Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp MET His Trp Val  
 CTG AAG GTG TCC TGC AAG GCC TCT GGC TAC ACC TTC ACC AGC TAC TGG ATG CAC TGG CTC  
 22 27 32 37 180  
 Lys Gln Arg Pro Gly Gln Gly Leu Asp Trp Ile Gly Glu Ile Asn Pro Ser Asn Gly Arg  
 AAG CAG AGG CCT GGA CAA GGC CTT GAC TGG ATT GGA GAG ATT AAT CCT AGC AAC GGT CGT  
 42 47 52 57 240  
 Thr Asn Tyr Asn Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser  
 ACT AAT TAC AAT CAG AAG TTC AAG AGC AAG GCC ACA CTG ACT GTA GAC AAA TCC TCC AGC  
 62 67 72 77 300  
 Thr Ala Tyr MET Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala  
 ACA GCC TAC ATG CAA CTC AGC AGC CTG ACA TCT GAG GAC TCT CCG GTC TAT TAC TGT GCC  
 82 87 92 97 360  
 Ser Tyr Asp Tyr Asp Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 TCC TAT GAT TAC GAC TGG TTT GCT TAC TGG GGC CAA GAG ACT CTG GTC AC<sub>2</sub>GTC TTC TCA  
 102 107 112 117\* 420  
 375 390 405

BsvET

FIG.12B

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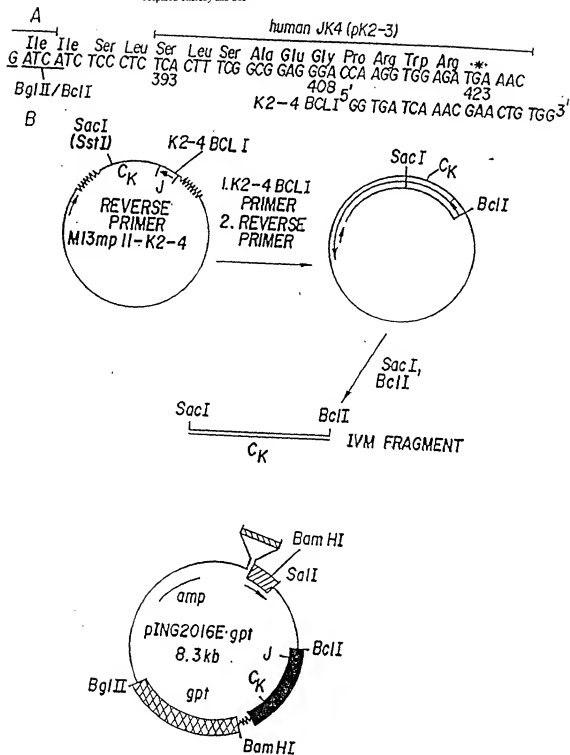


FIG. 13

10040945-010302

206010-5460400T

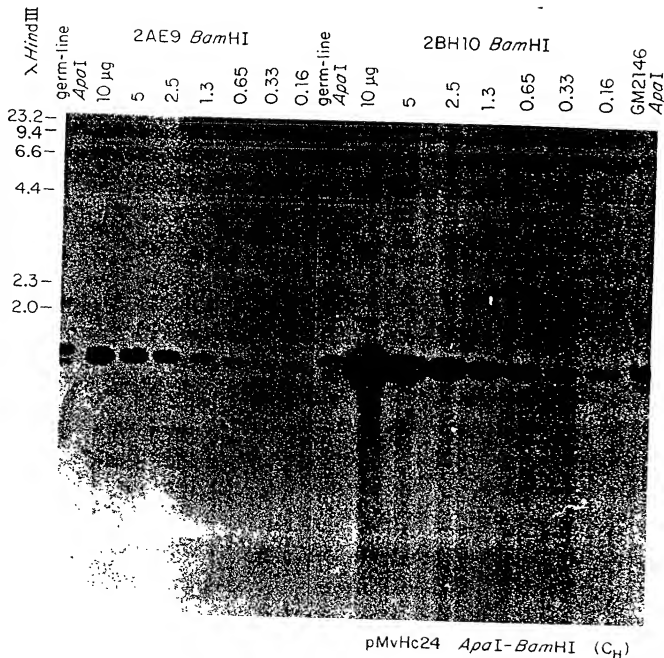


FIG. 14

[illegible][illegible]

FIG. 15

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MET Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser Val Ile MET Ser Arg Gly Gln  
 CCC CCC CCC CCA GAC AAA ATG GAT TTT CAA CTG CAG ATT TTC AGC TTC CTG CTA ATC ATG GGT TCA GTC ATA ATG TCC AGA GGA CAA 90  
 15 30 45 60 75  
 Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Phe  
 ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT CCA TCT CCA GGG GAG AAG GTC ACA TTG ACT TGC AGG GCC AGC TCA AGT GTA AGT TTC 180  
 105 120 135 150 165  
 COR1-FRI  
 MET Asn Trp Tyr Gln Gln Lys Pro Gly Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Glu Phe Pro Gly Arg Phe  
 ATG AAC TGG TAC CAG CAG AAG CCA GCA TCC TCC CCC AAA CCC TGG ATT TAT GCC ACA TTT GCT TCT GGT TCC CCG TCC GGT CCG TTC 270  
 195 210 225 240 255  
 Ser Gly Glu Trp Ser Gly Thr Ser Tyr Ser Leu Ala Ile Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Asn  
 AGT GGC GAG TGG TGT GGG ACC TCT TAC TCT CTC GCA ATC AGC AGA GTG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG AAT 360  
 285 300 315 330 345  
 COR3-FRI  
 Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Lys Lys Arg  
 ACT AAC CCA CTC ACC TTC GGT GCT GGG ACC AAG CTG CAG CTG AAA CCG 405  
 375

Hind III PRIMER

V<sub>K</sub> J<sub>K</sub> C<sub>K</sub> An  
 —————→

Bam HI H<sub>2</sub>O

pL3-120

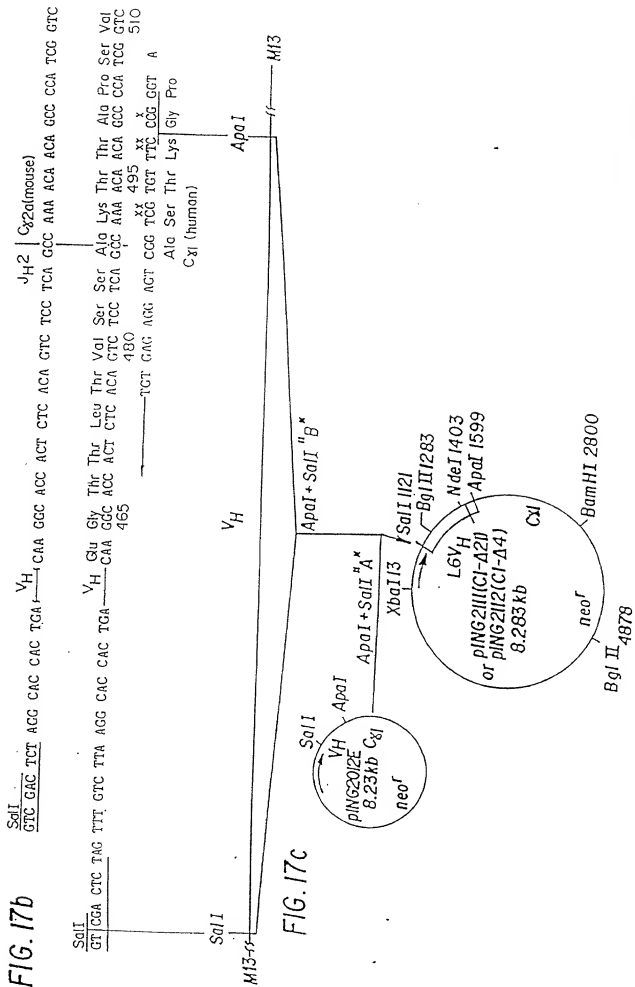
100bp

FIG.16

206010-51604001

BamHI  
 L6VH GG ATC CCC CCC CCC CCC CCC CAG TTT GTC TTA AGG CAC CAC TGA GCC CAA CTC TTA GAC ATC ATG GAT TGG CTG TGG AAC Leu  
 PH3-6q 5 17 32 47 62  
 MET Asp Trp Leu Trp Asn Leu  
 Cl-44  
Sall  
CTC GAC TCT AGG CAC CAC TGA GCC CAA CTC TTA GAC ATC ATG GAT TGG CTG TGG AAC TTG  
 Cl-Δ21  
Sall  
GT CGA CTC TAG TTT GTC TTA AGG CAC CAC TGA GCC CAA CTC TTA GAC ATC ATG GAT TGG CTG TGG AAC TTG

FIG. 17a



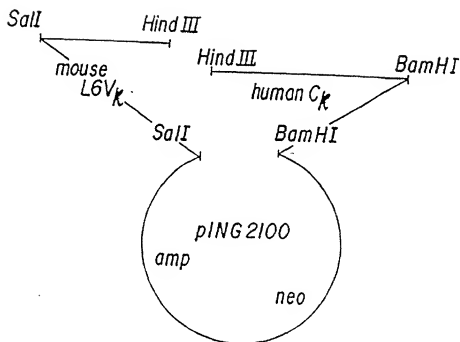


FIG. 18

1040945-010302



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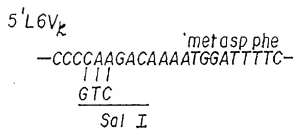


FIG.19A

20040915-010902

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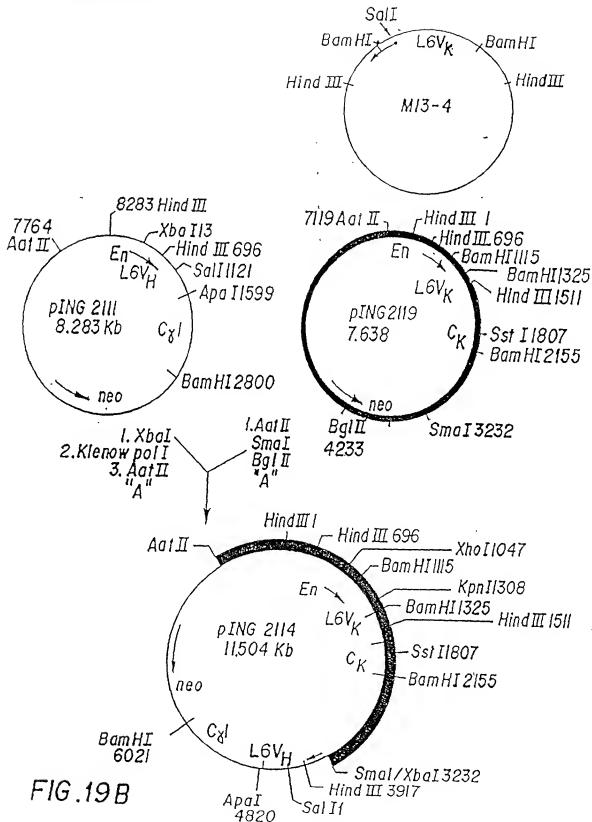


FIG. 19B

10040945.010902

206010-51604001

# L6 Chimerae

$V_H$  pH3-6A ( $V_H^2$ ) oligo (dT) clone, BAL -31 deletions 5' Cx1 APA mutagenesis  $\rightarrow$  pING 2111 neo

pING 2112 neo

Sall  $\downarrow$  pING2111 pING2112  $\downarrow$

5' GTCGACTCTAGTITGTCTTAAAGGCACCACTGAGCCCAAG

met  
TCCTTAGACATCATGGAT

joint ACC ACT CTC ACA GTC TCC TCA | GCC AGC ACA AAG GGC  
 ApaI  $\downarrow$   
 C CAT

mo | hu

$V_K$  p13-12A ( $V_K^5$ ) oligo (dT) clone, J $\kappa$ Hind III mutagenesis, 5' SAL mutagenesis  $\rightarrow$  pING 2119 neo  
 pING 2120 got

Sall  $\downarrow$  met

5' GTC GAC AAA ATG GAT

joint ACC AAG CT  $\odot$  GAG  $\odot$  ATG AAA | CGA ACT  
 mo  $\downarrow$  hu  $C_K$

FIG.20

2H7 heavy chain variable sequence

leader

C<sub>33</sub>GTACCTCTCTACAGTCCCTGAAGACACTGACTCTAA<sup>met gly phe ser arg ile phe</sup>  
<sup>peptide</sup>CCATG GGA TTC AGC AGG ATC TTT  
 leu phe leu leu ser val thr thr gly val his ser<sup>gln ala tyr leu gln</sup>  
 CTC TTC CTC CTG TCA GTA ACT ACA GGT GTC CAC TCC CAG GCT TAT CTA CAG

gln ser gly ala glu leu val arg pro gly ala ser val lys met ser cys  
 CAG TCT GGG GCT GAG CTG GTG AGG CCT GGG GCC TCA GTG AAG ATG TCC TGC

lys ala ser gly tyr thr phe thr<sup>FR1</sup> ser tyr asn met his trp val lys gln  
 AAG GCT TCT GGC TAC ACA TTT ACC AGT TAC AAT ATG CAC TGG GTA AAG CAG

thr pro Qrg gln gly leu glu trp ile gly ala ile tyr pro gly asn gly  
<sup>FR2</sup>ACA CCT AGA CAG GGC CTG GAA TGG ATT GGA GCT ATT TAT CCA GGA AAT GGT

asp thr ser tyr asn gln lys phe<sup>CDR2</sup> lys ala thr leu thr val asp  
 GAT ACT TCC TAC AAT CAG AAG TTC AAG GGC AAG GCC ACA TCG ACT GTA CAG

lys ser ser ser thr ala tyr met gln leu ser ser leu thr ser glu asp  
 AAA TCC TCC AGC ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAA GAC

ser ala val tyr phe cys ala arg<sup>FR3</sup> val val tyr tyr ser asn ser tyr trp  
 TCT GCG GTC TAT TTC TGT GCA AGA GTG GTG TAC TAT AGT AAC TCT TAC TGG

tyr phe asp val<sup>CDR3</sup> trp gly thr gly thr thr val thr val ser<sup>FR4</sup>  
 TAC TTC GAT GTC TGG GGC ACA GGG ACC ACG GTC ACC GTC TCG<sup>30</sup>

↓  
Bst EI

J<sub>H</sub>Bst EII primer

FIG. 21

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2H7 light chain variable sequence

leader peptide

met asp phe gln val gln ile phe ser phe leu leu  
C<sub>23</sub> CCCCAAATTCAAAGACAAATG GAT TTT CAA GTG CAG ATT TTC AGC TTC CTG CTA  
GTC SalI primer FRI  
ile ser ala ser val ile ile ala arg gly gln ile val leu ser gln ser  
ATC AGT GCT TCA GTC ATA ATT GCC AGA GGA CAA ATT GTT CTC TCC CAG TCT  
pro ala ile leu ser ala ser pro gly glu lys val thr met thr cys arg FRI  
CCA GCA ATC CTG TCT GCA TCT CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG  
CDR1  
ala ser ser ser val ser tyr met his trp tyr gln gln lys pro gly ser  
GCC AGC TCA AGT GTA AGT TAC ATG CAC TGG TAC CAG CAG AAG CCA GGA TCC  
FR2, CDR2 KpnI  
ser pro lys pro trp ile tyr ala pro ser asn leu ala ser gly val pro  
TCC CCC AAA CCC TGG ATT TAT GCC CCA TCC AAC CTG GCT TCT GGA GTC CCT  
CDR2, FR3 BamHI  
ala arg phe ser gly ser gly ser gly thr ser tyr ser leu thr ile ser  
GCT CGC TTC AGT GGC AGT GGG TCT GGG ACC TCT TAC TCT CTC ACA ATC AGC  
FR3, CDR3  
arg val glu ala glu asp ala ala thr tyr tyr cys gln gln trp ser phe  
AGA GTG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG AGT TTT  
CDR3, FR4 J<sub>H</sub>  
asn pro pro thr phe gly ala gly thr lys leu glu leu lys FR4  
AAC CCA CCC ACG TTC GGT GCT GGG ACC AAG CTG GAG CTG AAA  
J<sub>H</sub> HIND III primer

FIG. 22

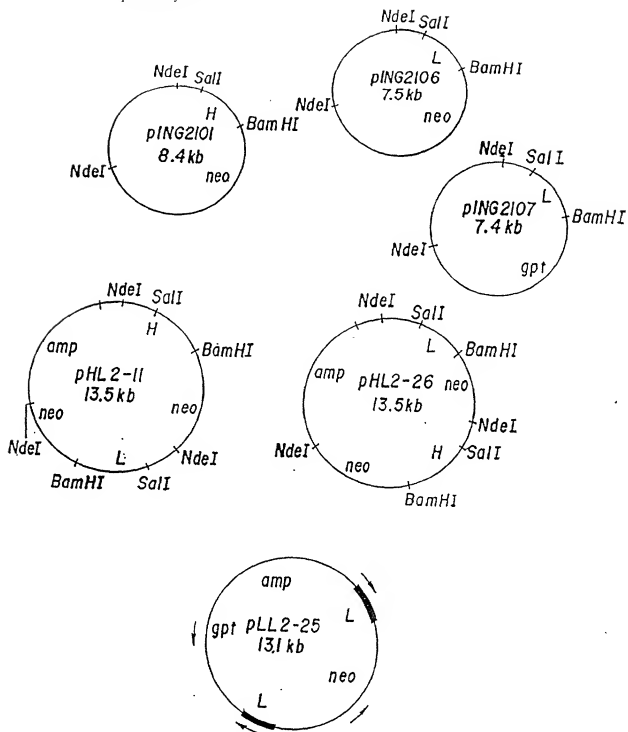


FIG. 23

2H7 Chimerae

V<sub>H</sub> pH2-7 (J<sub>H</sub>1) J<sub>H</sub>BstEII clone, NcoI cut 5'ATG → pING2101 neo

5' SalI met  
 ↓  
 GTC GACATG GGA

joint mo, hu  
 ↓  
 ACGGTC ACC GTC TCC TCA GCC TCC CxI

V<sub>K</sub> pL2-12 (J<sub>K</sub>5) oligo(dT) clone, J<sub>K</sub>HindIII mutagenesis, 5' SAL mutagenesis → pING2106neo  
 pING2107 gpt

5' SalI met  
 ↓  
 GTC GAC AAA ATG GAT

joint neo, hu  
 ↓  
 ACC AAG CT GAG ATG AAA CGA ACT CK

FIG. 24

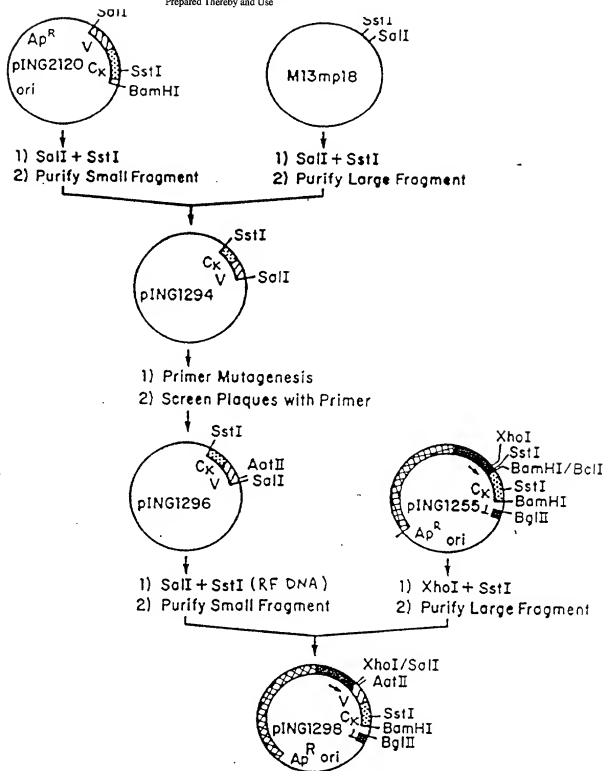


FIG. 25A



206010\* 51601007

Signal Sequence  
Processing Site

MET Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser Val Ile MET Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala  
ATG CAT TTT CAA GTG CAG ATT TTC AGC TTC CTG CTA ATC AGT GCT TCA GTC ATA ATG TCC AGA GCA CAA ATT GTT CTC TCC CAG TCT CCA GCA  
5' ATA ATG TCC CAA GCT CAA ATT GTT 3'  
AotII

FIG.25B

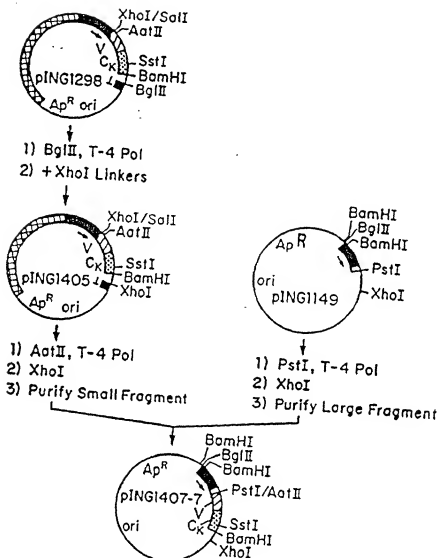


FIG.25C

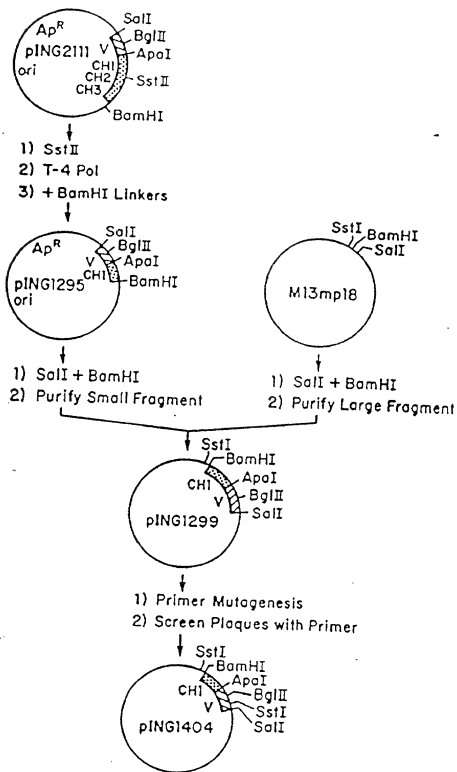


FIG. 26A

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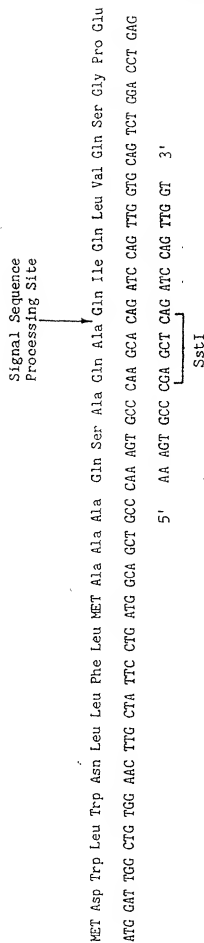


FIG. 26B

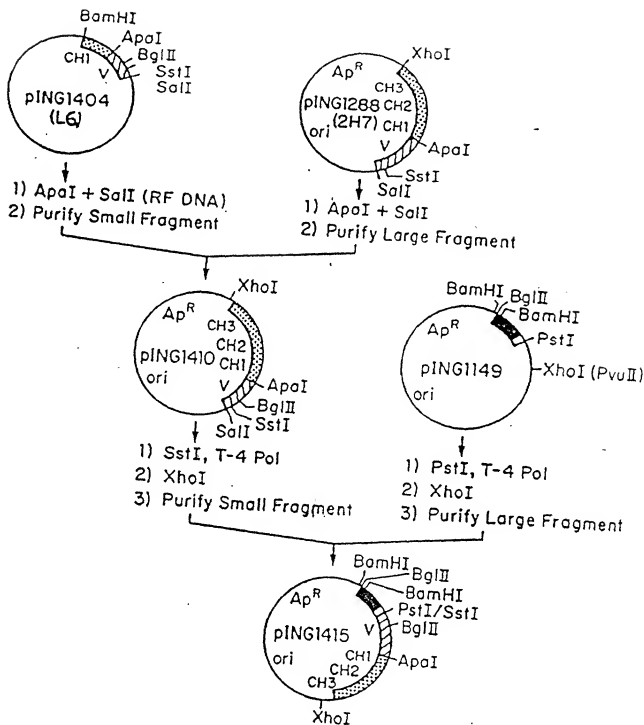


FIG.26C

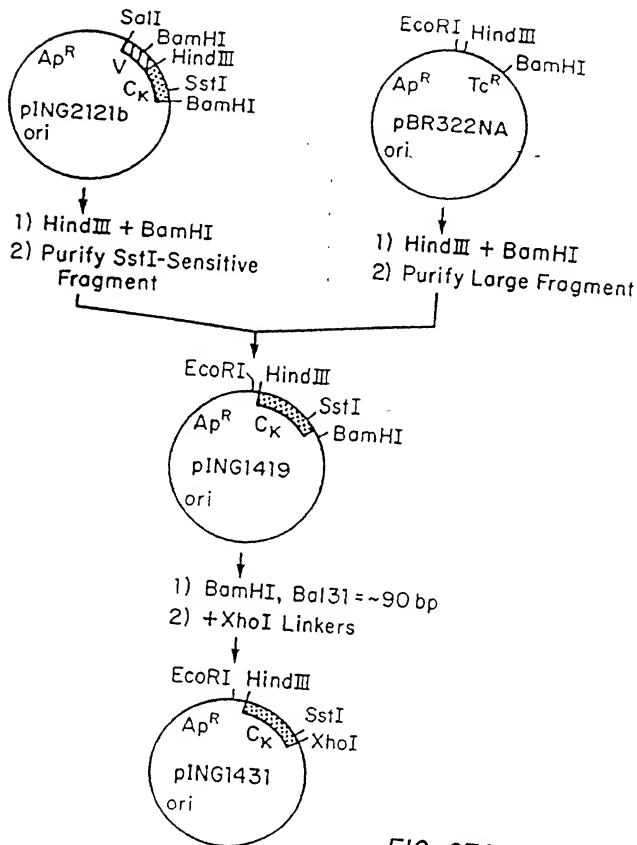


FIG. 27A

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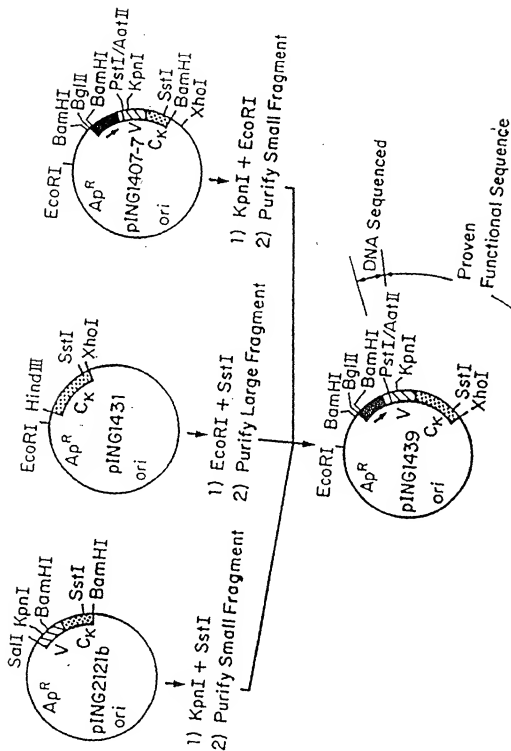


FIG. 27B

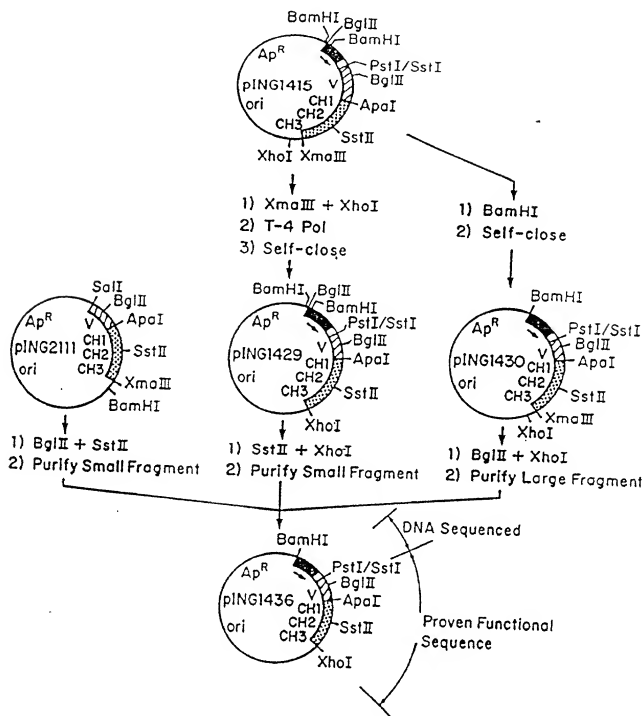


FIG.28



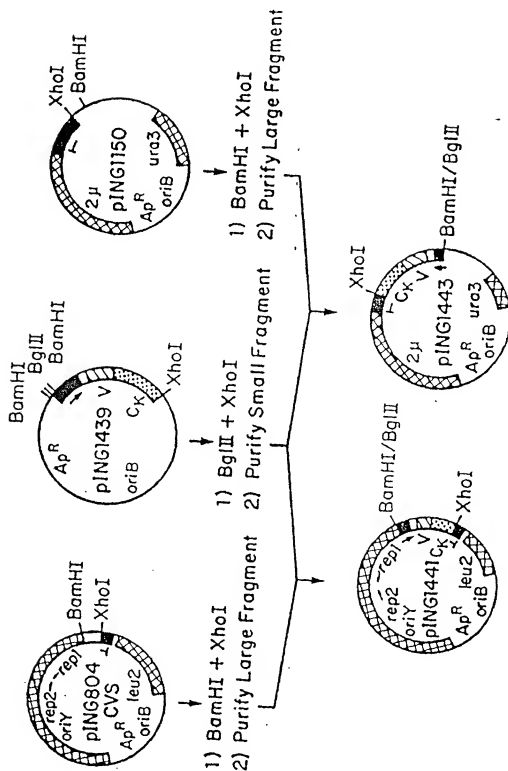


FIG. 29

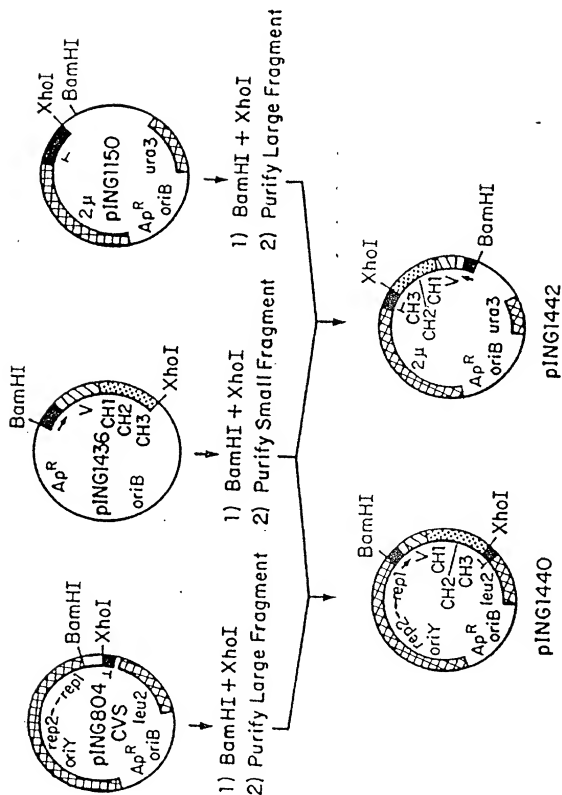


FIG. 30



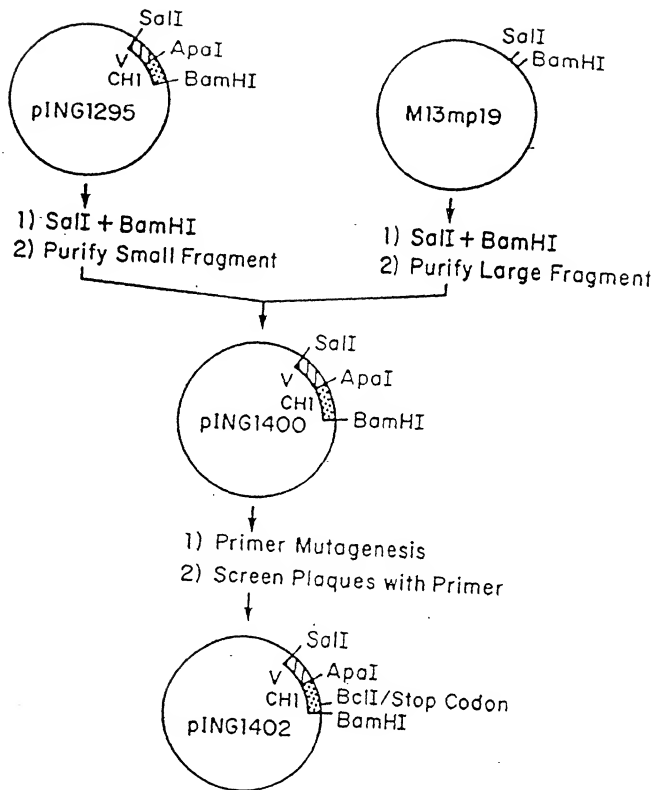


FIG. 32A

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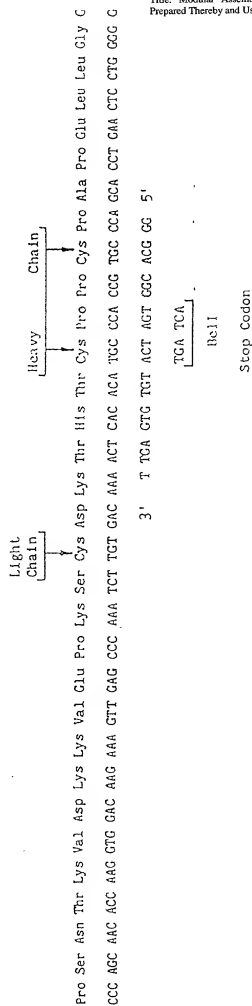


FIG. 32B

206610-54607007

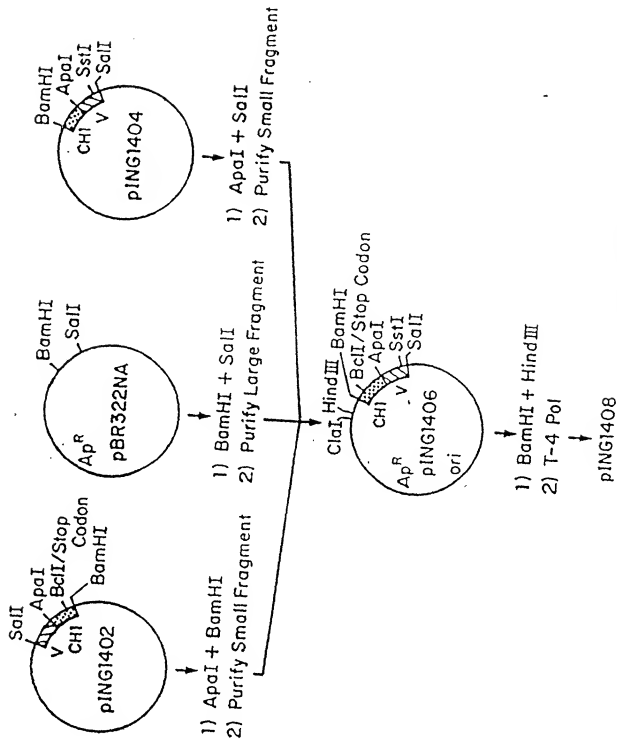


FIG. 33A

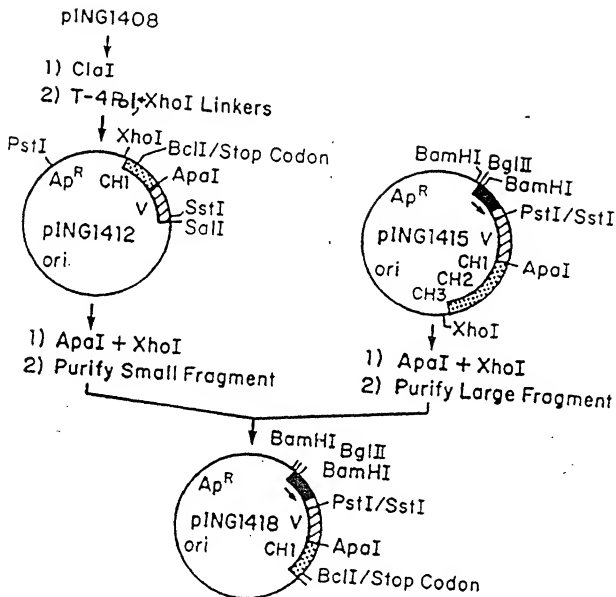


FIG. 33B

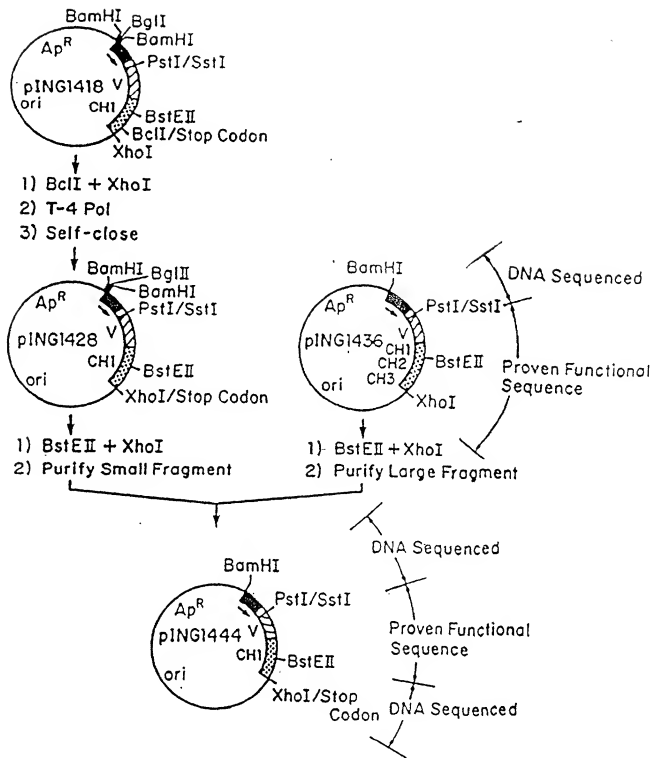


FIG. 34



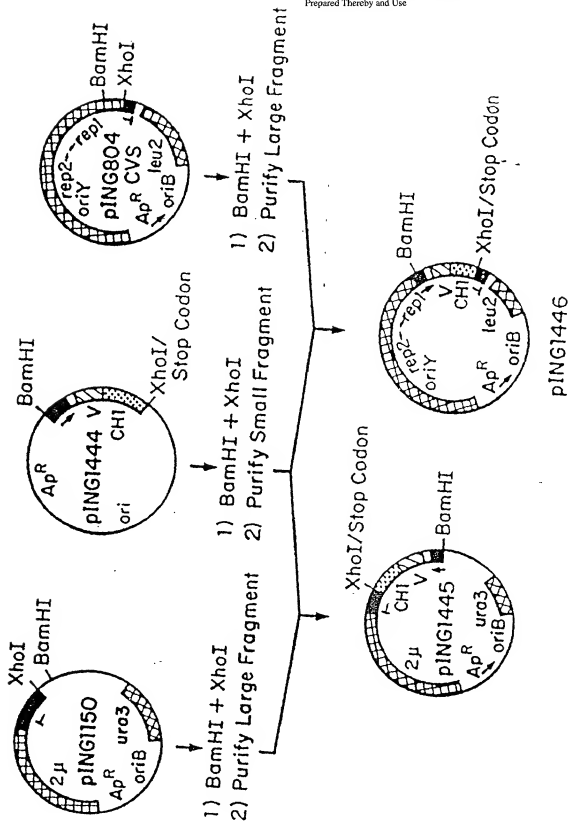


FIG. 35

TTT AAA AGG AAA TTT TTT CTT ATA AAA

CCC AAA TTA TCC AAT CAT CAG TAT TAC AAA ATG TTT CAA CCG TAA TAC ATT TAA CAT TTC

ACC CTT GAA CTG ATC TTA TTT TTT GAC CAC AÇT CCC CTT GGT TTT TCA CCA AAA CTG AGT

Nde I

TTC ATT TTT GTT GAA AAA TTT GTA CCT GCG ACA TCG GGC ATA TGG AAC GAT AAA TGC CCA

1

TGA AAA TTC TAT TTC AAG GAG ACA GTC ATA ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT MET Lys Tyr Leu Leu Pro Thr Ala Ala Ala

Hoe III

Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala MET Ala Ala Asn Thr Gly Gly Tyr Ala Thr  
GGA TTG TTA TTA CTC GCT GCC CAA CCA GCG ATG GCC GCA AAT ACG GGT GGC TAT GCC ACC

FIG. 36 A

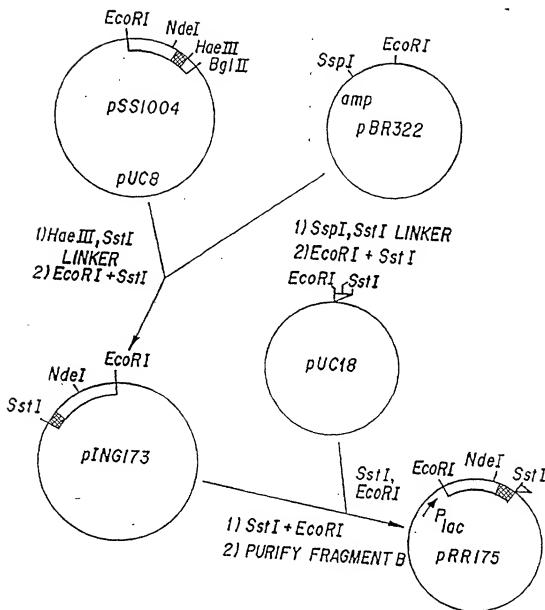


FIG. 36B

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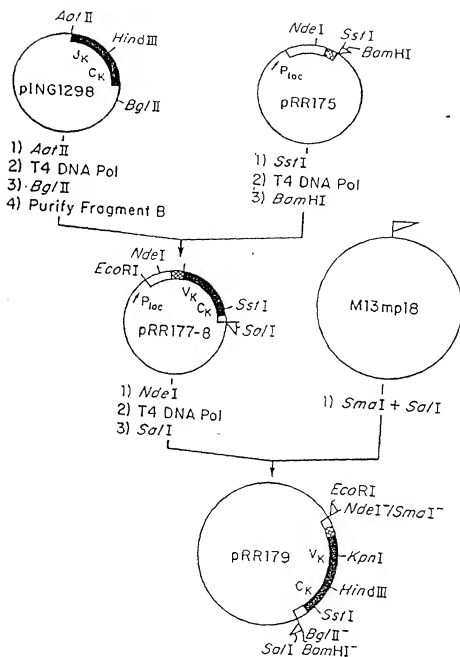


FIG. 37A

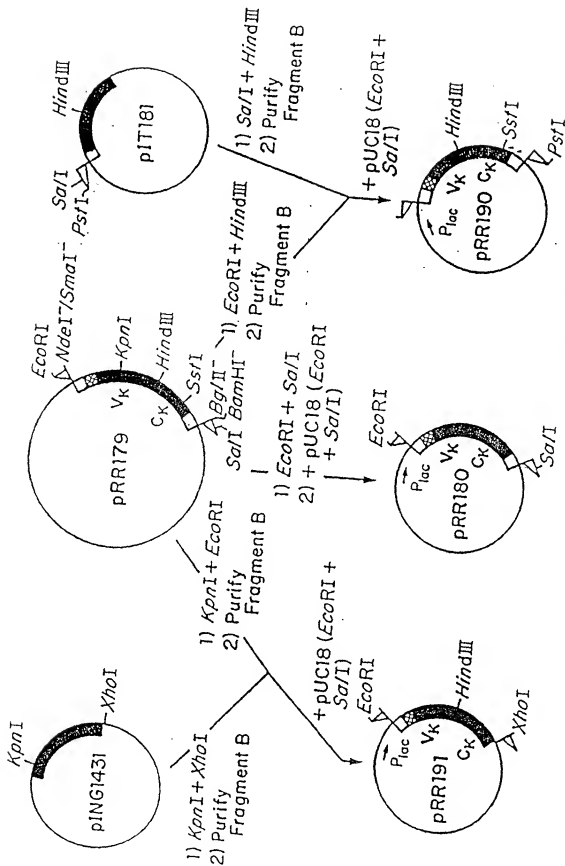


FIG. 37B

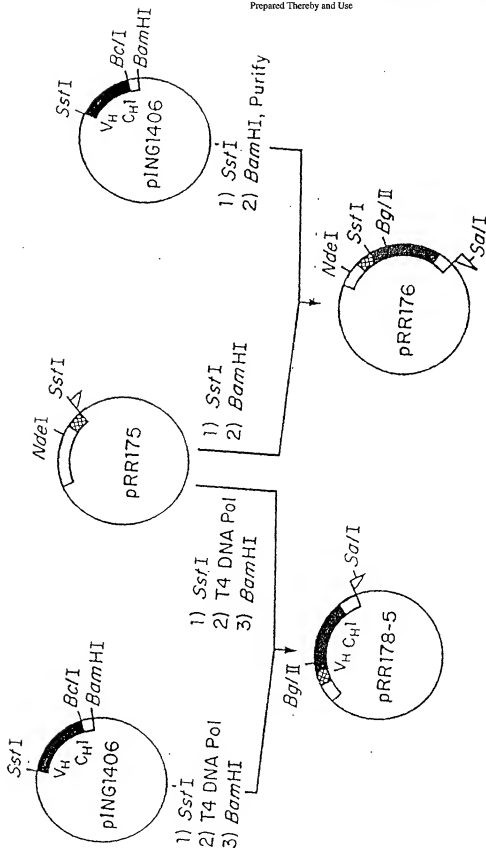


FIG. 38A

206070-54604001

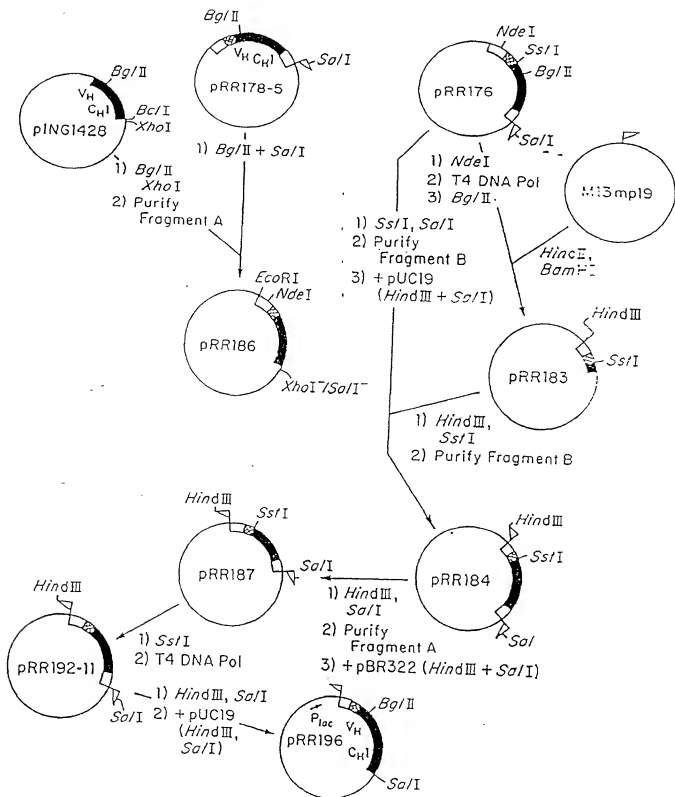


FIG. 38B

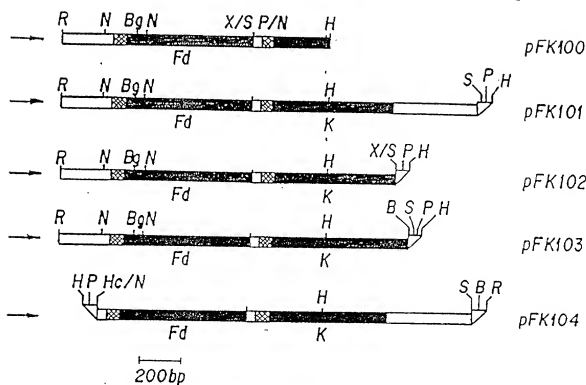


FIG. 39



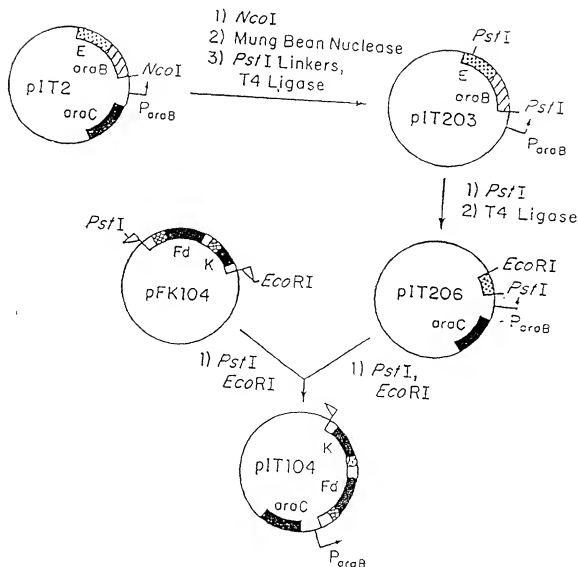


FIG. 40A

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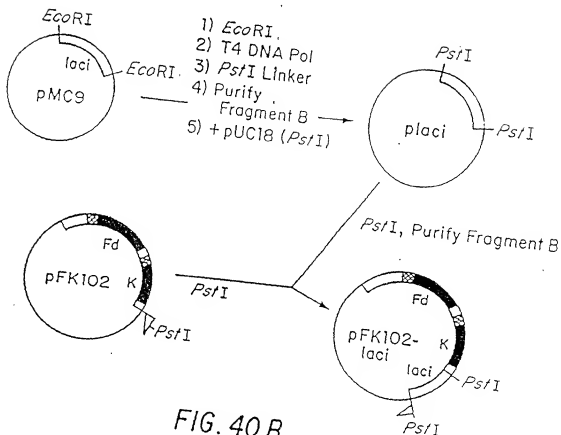


FIG. 40 B

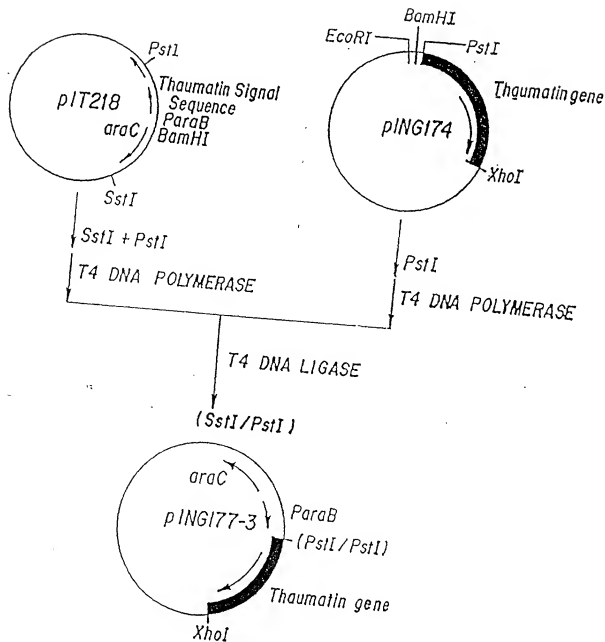


FIG. 41

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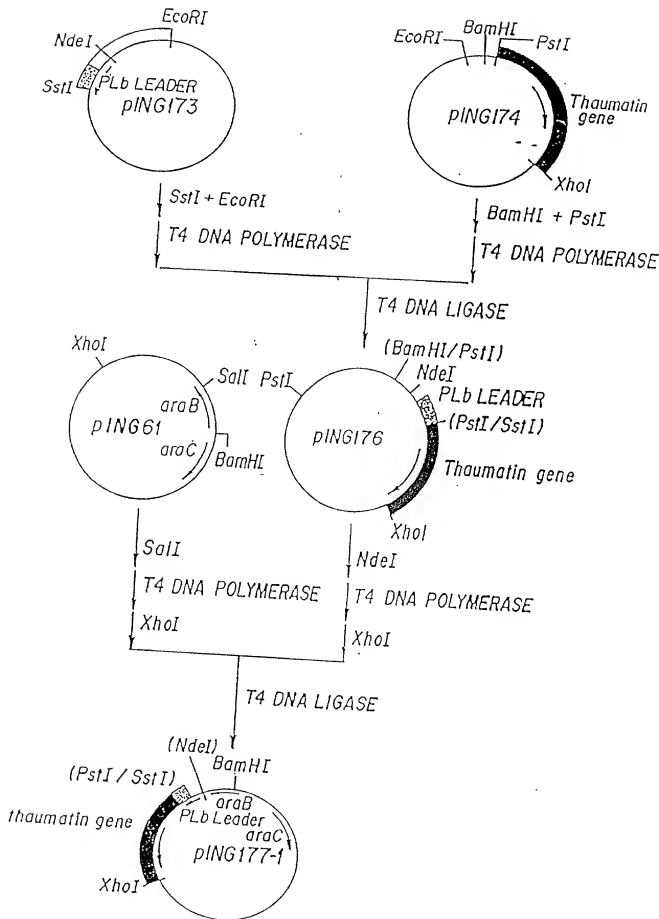


FIG. 42

10040945.010902

